

CLUSTAL W (1.82) multiple sequence alignment

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Eamylovora_HrpW      ATGTCAATTCTTACGCTTAACAACAATACCTCGTCCTCGCCGGGTCTGTTCCAGTCCGGG 6
Epyrifoliae_HrpW    ATGTCAAGTTCTTACGCTTAACATCAGTATCCCGTCTCGCAGGGGCTATTCAAGCCCCGC 6
*****

Eamylovora_HrpW      GGGGACAACGGGCTTGGTGGTCATAATGCAAATTCTGCGTTGGGGCAACAACCCATCGAT 1
Epyrifoliae_HrpW    GAAGACAACGGACTTAGTGGTCAAATACAAATTCAGCACAGGGGCGACCCCCATCGAT 1
* *****

Eamylovora_HrpW      CGGCAAACCATTGAGCAAATGGCTCAATTATTGGCGGAACGTGTTAAAGTCACTGCTATCG 1
Epyrifoliae_HrpW    CGGCAAACCATTGAGCAAATGGCGCAATTATTGGGAGAACGTGTTAAAGCCGCTGCTATCG 1
*****

Eamylovora_HrpW      CCACAATCAGGTAATGCGGCAACCGGAGCCGGTGGCAATGACCAGACTACAGGAGTTGGT 2
Epyrifoliae_HrpW    CCACAGGCAGATAATGCAGCA-----GCAGGTAGCAATGACCAGACCAACGGAGTGGGC 2
*****

Eamylovora_HrpW      AACGCTGGCGGCCTGAACGGACGAAAAGGCACAGCAGGAACCACTCCGCAGTCTGACAGT 3
Epyrifoliae_HrpW    AACGCTGGCGGCCTGACGGGGCAAATGGCGCAGCAGGGACTACCCCGCAGTCTGTCAAC 2
*****

Eamylovora_HrpW      CAGAACATGCTGAGTGAGATGGGCAACAACGGGCTGGATCAGGCCATCACGCCCCGATGGC 3
Epyrifoliae_HrpW    CAGACAATGCTGGGTGAGATGGGCAATAACGGGCTGGATCAGGCCATCACGCCCCGATGGC 3
****

Eamylovora_HrpW      CAGGGCGGCGGGCAGATCGGCGATAATCCTTTACTGAAAGCCATGCTGAAGCTTATTGCA 4
Epyrifoliae_HrpW    CAGGGCGGCGGGCAGATCGGCGATAATCCTTTACTGAAAGCCATGCTAAAGCTTATCGCG 4
*****

Eamylovora_HrpW      CGCATGATGGACGGCCAAAGCGATCAGTTTGGCCAACCTGGTACGGGCAACAACAGTGCC 4
Epyrifoliae_HrpW    CGCATGATGGACGGGCAAAGTGACACGTTCCGGCCAGCCGGGATCCGGCAATAATGATGCG 4
*****

Eamylovora_HrpW      TCTTCCGGTACTTCTTCATCTGGCGGTTCCCCTTTTAACGAT-----CTAT 5
Epyrifoliae_HrpW    TCTTCCGGCCCTTCTTCGGCGGGGAATTATCCTGCCAGCAACGCGTCTTCTGGCTCTTCT 5
*****

Eamylovora_HrpW      CAGGGGGGAAGGCCCT-TCCGGCAACTCCCCTTCCGGCAACTACTCTCCCGTCAGTACC 5
Epyrifoliae_HrpW    CTCGGGGGAAGTTCTCTGTAGGTAAAGCGTCTTCTGGCGGCACATCTCCACCAATTCC 5
* *****

Eamylovora_HrpW      TTCTACCCCCATCCACGCCAACGTCCCCTACCTACCGCTTGATTTCCCTTCTTCTCCC 6
Epyrifoliae_HrpW    TTCTACCAACCGTCCACGCCGACCTCCCCACCTACCGCTTGATTTCCCTTCTTCCCC 6
*****

Eamylovora_HrpW      ACCAAAGCAGCCGGGGGCGAGCAGCCGGTAACCGATCATCCTGACCCTGTTGGTAGCGCG 7
Epyrifoliae_HrpW    ACCAGCGGTGCCGGGGGCGAGCAGCCGGTCACCGATCATGCTGACCCTGTCGGCAGTACC 7
****

Eamylovora_HrpW      GGCATCGGGGCCGGAAATTCGGTGGCCTTACCAGCGCCGGCGCTAATCAGACGGTGCTG 7
Epyrifoliae_HrpW    GGCGTGGGGGCCGGAAATTCGGTGGGCTTTACCAGCGCCGGCGCTAACCCGACTGTGCTG 7
***

Eamylovora_HrpW      CATGACACCATTACCGTGAAAGCGGGTCAGGTGTTGATGGCAAAGGACAAACCTTCACC 8
Epyrifoliae_HrpW    CATGACACCATCATCGTAAAGCGGGTCAGGAGTTTATGGCAAAGGGCAAACCTTCACC 8
*****

Eamylovora_HrpW      GCCGGTTCAGAATTAGGCGATGGCGGCCAGTCTGAAAACAGAAACCGCTGTTTATACTG 8
Epyrifoliae_HrpW    GCCGGTTCAGAATTAGGCGATGGCGGCCAGTCTGGAAGCCAGAAGCCGCTGTTTATGCTG 8
*****

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Eamylovora_HrpW	GAAGACGGTGCCAGCCTGAAAAACGTCACCATGGGCGACGACGGGGCGGATGGTATTCAT	9
Epyrifoliae_HrpW	GAAGACGGTGCCAGCCTGAAAAACGTCACCATCGGCGATGATGGGGCGGATGGCATTTCAT	9

Eamylovora_HrpW	CTTTACGGTGATGCCAAAATAGACAATCTGCACGTCACCAACGTGGGTGAGGACGCGATT	1
Epyrifoliae_HrpW	CTTTACGGTGATGCCAAAATAGACAATCTGCACGTCACCAACGTGGGAGAGGACGCGATA	1

Eamylovora_HrpW	ACCGTTAAGCCAAACAGCGCGGGCAAAAAATCCCACGTTGAAATCACTAACAGTTCCTTC	1
Epyrifoliae_HrpW	ACCGTTAAGCCAAACAGCGCTGGCAAAAAATCTCACGTTGACATCACCAACAGCTCCTTT	1

Eamylovora_HrpW	GAGCACGCCTCTGACAAGATCCTGCAGCTGAATGCCGATACTAACCTGAGCGTTGACAAC	1
Epyrifoliae_HrpW	GAGCACGCCTCTGACAAGATCCTGCAGCTGAATGCTGATACCACCCTGAACGTTGACAAC	1

Eamylovora_HrpW	GTGAAGGCCAAAGACTTTGGTACTTTTGTACGCACTAACGGCGGTCAACAGGGTAACTGG	1
Epyrifoliae_HrpW	GTGAAGGCCAAAGACTTTGGTACTTTTCGTACGCACTAACGGAGGTCAACAGGGTAACTGG	1

Eamylovora_HrpW	GATCTGAATCTGAGCCATATCAGCGCAGAAAGACGGTAAGTTCTCGTTCGTTAAAAGCGAT	1
Epyrifoliae_HrpW	GATCTGAATCTGAGCCATATCAGCGCAGAGAACGGTAAATTCTCGTTCGTTAAAAGCGAT	1

Eamylovora_HrpW	AGCGAGGGGCTAAACGTCAATACCAGTGATATCTCACTGGGTGATGTTGAAAACCACTAC	1
Epyrifoliae_HrpW	AGCGAGGGGCTAAACGTCAATACCAGTGATATCTCACTGGGCAACGTTGAAAACCACTAT	1

Eamylovora_HrpW	AAAGTGCCGATGTCCGCCAACCTGAAGGTGGCTGAATGA	1344
Epyrifoliae_HrpW	AAAGTGCCGATGTCCGCCAATCTGAAGGTGGCTAAATGA	1353

CLUSTAL W (1.82) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: Eamylovora_HrpW 1344 bp

Sequence 2: Epyrifoliae_HrpW 1353 bp

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 86

Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-2

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:22855

Alignment Score 8504

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-200